

BIO TECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09 763 011A

Source:

PCT 09

Date Processed by STIC:

11/14/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> 09/76301/A
ATTN: NEW RULES CASES: PLEASE DISREGARD ENCLISII "ALPIIA" IIHEADERS, WHICH WERE INSERTED BY P		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number(s) at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 3 rd amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length.	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <210>.<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <210>.<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <210>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <210>.<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (1) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (ii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: <210> sequence id number <400> sequence id number 000	
10 <input type="checkbox"/> Invalid <213> Response	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents	
11 <input type="checkbox"/> Use of <220>	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>.<223> section is required when <213> response is Unknown or Artificial Sequence	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
13 <input type="checkbox"/> Misuse of n	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	



PCT09

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/763,011A

DATE: 11/14/2001
TIME: 13:52:05

Input Set : A:\JAB-1415.txt
Output Set: N:\CRF3\11142001\I763011A.raw

5 <110> APPLICANT: Contreras, Roland
6 Nelissen, Bart
7 DeBacker, Marianne
8 Luyten, Walter
9 Viaene, Jasmine
10 Loghe, Marc George
13 <120> TITLE OF INVENTION: Drug Targets In Candida Albicans
16 <130> FILE REFERENCE: 50899/002
19 <140> CURRENT APPLICATION NUMBER: US/09/763,011A *✓*
21 <141> CURRENT FILING DATE: 2001-02-14
24 <150> PRIOR APPLICATION NUMBER: 98310694.9
26 <151> PRIOR FILING DATE: 1998-12-23
29 <150> PRIOR APPLICATION NUMBER: 9817796.7
31 <151> PRIOR FILING DATE: 1998-08-14
34 <160> NUMBER OF SEQ ID NOS: 114
38 <170> SOFTWARE: PatentIn Ver. 2.0
42 <210> SEQ ID NO: 1
44 <211> LENGTH: 1851
46 <212> TYPE: DNA
48 <213> ORGANISM: Candida albicans
52 <400> SEQUENCE: 1
54 atgtcattag ataattcaac agaaaaccgt gatttggaaag aaaaggaaaga aat
56 aacgaacata acgaacaagg cgaacaaaac gagaacaatg agcatatacc tac
58 gataaaccat tgaaggaata tattggatt agtattttgt gtttccttat tgc
60 ggtttcggtt ttggttcga tactggtacc atttctgggt tcattaacat gac
62 ttagaaagat ttgggtgtac taaagctgac ggtactcttt acttttccaa cgt
64 ggtttattga ttggttgtt caatgtgggt tgcgcatttgcgttgcatttattttt
66 gtcggtgata tgtacgttag aagagttgggt atcatgactg ctatgatcat ttat
68 ggtattatttg ttcaaaattgc ttctcaacat gcttgggtatc aaatcatgtat tgg
70 atcaactggtc ttgctgttgg tatgttatca gttttgtgtc cattattttat ctc
72 tctcccaaaccat atttaagagg tacatttagtt tattgtttcc aatttgatgtat tac
74 attttcttgg gttactgtac cagttacgggt actaagaat attctgactc cag
76 agaattccat tgggtttatg ctttgcttgg gccttgggt tgcttgggtt tatt
78 atgccagaat ctccacgtta ctttgcgtt aaagatagaa ttgacgtatgc taat
80 cttgccccaaaa ctaacaaggt ttctccagag gaccctgtat tataccgtat act
82 atccaagctg gtgttggaaag agaaaagattt gcccggtaagg catcttgggg tgg
84 actggtaaac caagaatcct tggaaagagtt attgttggag gtatgttgc atcc
86 caattgactg gtgataacta ttctttctac tacagttacca ccattttcaat gtc
88 ttaaatgatt ctttcgaaac atctattatc ttgggtgtca tcaactttgc ttat
90 gttgggtatccat atgccatttga aagattgggtt agaagactttt gtttattaaac tgg
92 gccatgtcca ttgtttctt aatttactca ttgattggta ctcaacatct ttaat
94 caaccaggtt gtcacccatg aaaaccatgat ggtacgtat tgattttcat tac
96 tatgttttctt tcttcgttac tacatgggtt ggtgggtctt actccattgtt ttc
98 tatccattaa aagtccagaag taaggctatg gttttgtatc atgcatgtaa ctg
100 gttttcttgc ttcccttctt cacttcattt atcaactgtatg ctatccactt ct
102 ttgtgttta tgggtgtttt agtgtttcc atttcttttgc tttactttat gat
104 actaaaggatgc ttacttttgc qgaaattgtat gattataact ctaccaaggat tgg

**Does Not Comply
Corrected Diskette Needed**

RAW SEQUENCE LISTING

DATE: 11/14/2001
TIME: 13:52:05

Input Set : A:\JAB-1415.txt
Output Set: N:\CRF3\11142001\I763011A.raw

106 aaatcagccg gttgggttcc accttctgac gaagaaaatgg ttctgtgc aaaaaggctataact 1620
108 ggtgatatacc acgcagatga agagcaagtt taatcaactc ttgtcaatt aatgctgtac 1680
110 ttgtttcat ttatgttgc ggcatttaaa gaataccccat agttcagaaaa ataaaatttga 1740
112 aaaatttaaa aaaaaacgca atatcattca tttttttgt ttttttgaca ataataattaa 1800
114 tatgttagtta ccaatgttt tagatttat atgtttgaa aaaatagttt g 1851
118 <210> SEQ ID NO: 2
120 <211> LENGTH: 648
122 <212> TYPE: DNA
124 <213> ORGANISM: Candida albicans
128 <400> SEQUENCE: 2
130 aacctttat tcgggtct tag tgcattcaatt ggttatccat taacatctat tcccaactcc 60
132 atcattattt gcaataaaa aatgggtgtt atatctattt gtaataacta aactgggtgtc 120
134 aattcaattt caatatggtc atgacaattt aagtgttac ttgttctgggt tacatatttct 180
136 acagggttaca actattgtt ggttagaagt ttgtttcaat catcacctgt tgctaagaat 240
138 aaatgttggt catatcaattt gaatcattt ggtgttgc ggtaaatggaa tgctgggtt 300
140 atctattatc tacaaccacc aagtgtataaa tgctgaaccg tagtcacccaa ctgttatgtc 360
142 gggtgtatct attgactaaa actaccctag ggataaatgc tgaaccgtgg ttaccaactg 420
144 ttatgtcggt tgcattctt aactgcaacc accaaatgtt aaatgttgc ccataattac 480
146 caactgttac attgtcggtt ctacattaag aataaaatgtt gcatctacaa gtaccacactg 540
148 ttgtgttaat aaatgtcgca cctgttagt caactgttgc tggcatgtat agttactaca 600
150 cattacacac cagacagtgg caaaacaagg tatgttagaaa ccaacgtt 648
154 <210> SEQ ID NO: 3
156 <211> LENGTH: 1497
158 <212> TYPE: DNA
160 <213> ORGANISM: Candida albicans
164 <400> SEQUENCE: 3
166 gatatctgca gaattcggct tctctctcat cttcacacaa tgcattttac aagtagccta 60
168 ctagccacct tgcattgtt tacattaccg gttcaagtt tgaataactga atcttaggaca 120
170 acttcaaata acacaatatac aatacttaca aaccattttc aaatactaaa ggatttgctt 180
172 ccatatagca aaacttctaa accgcaatc aaggaatcca gaccgttgc taaagttctg 240
174 agagatggag tgccataaa tttccacagg gctccggcta taataatgaa atcgaacaaa 300
176 acagacgatt tagtcaggaa tagcaataaa acaatggtgc taactgaaat aaaaacgatt 360
178 actgaatttg caactaccac ttgttccctt acacaagaat ttcaagact acagataaaac 420
180 cttAACACGT tatcaataga gacttcaaca ccaacattcc aatcccattga ctttccaccc 480
182 attaccattt aagacacacc caaaacacta gaaccagaag aatcgtcaga tgctttgcag 540
184 agggatgcat ttgatcaat taagaaaacta gaaaaattgg tattggattt gagacttgg 600
186 atgaaagagc aacaaaagag ttcaacgtt caattgtgg atatataatac cgcaagaagt 660
188 attgttccaa ttatgttac acatatcgtc acttcggcga ttccatcgta ttttccaccc 720
190 gaagaagttaa tggtttcaca tgatactgca ccaattgtaa gtcgtccctag aacagatatt 780
192 ccagtatctc aacgaatttga tactatctca aaacataaaa tgaatggaaa aaatataattt 840
194 aacaacaatc ctccggccaa ttctgttttta atagttcctc agtttcaagtt ccatgaaaga 900
196 atggccacca aaaccgaagt agcttataatg aaaccaaaaa ttgtctggac caactttcca 960
198 accactactg caacgtcaat gttgacaat ttatgtttaa aaaatctgt tgacgaaacg 1020
200 gattctgaaa ttgatgtgg tggaaactgaa ttgtctgacg attatttata ctattatagt 1080
202 tacgaagatg atggtaaaga agacgtatgt gatgagatgtt cggctcaat actattatcc 1140
204 aattcagaat taggcacgaa gacgcaaat tttgaggatc ctttgcata aatcaatatt 1200
206 gaagacaata aagtaatatac tgtaataca ccaaaagacaa agaaacctac tacaacagta 1260
208 ttggcactt ctactgtgc attatcaact tttgaaagta caatatttga aattcccaaaa 1320
210 ttctttatg ttagcagaag aaaacaactg agctcattca aaaataaqaa catgtacaatc 1380

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/763,011A

DATE: 11/14/2001
TIME: 13:52:05

Input Set : A:\JAB-1415.txt
Output Set: N:\CRF3\11142001\I763011A.raw

212 aaatttgatg tggttggatgg gatatttggaa agtggtaacta ccaatgagaa agtacatggaa 1440
 214 ttagtgttgg tgtctagtgg tggttctacta ggaacttgc tattgttcat tttgtag 1497
 218 <210> SEQ ID NO: 4
 220 <211> LENGTH: 485
 222 <212> TYPE: PRT
 224 <213> ORGANISM: Candida albicans
 228 <400> SEQUENCE: 4
 230 Met His Phe Thr Ser Ser Leu Leu Ala Thr Leu Ile Trp Phe Thr Leu
 232 1 5 10 15
 236 Pro Val Gln Ser Leu Asn Thr Glu Ser Arg Thr Thr Ser Asn Asn Thr
 238 20 25 30
 242 Ile Ser Ile Leu Thr Asn His Phe Gln Ile Leu Lys Asp Leu Leu Pro
 244 35 40 45
 248 Tyr Ser Lys Thr Ser Lys Pro Gln Ile Lys Glu Ser Arg Pro Leu Ile
 250 50 55 60
 254 Lys Val Ser Arg Asp Gly Val Pro Ile Asn Phe His Arg Ala Pro Ala
 256 65 70 75 80
 260 Ile Ile Met Lys Ser Asn Lys Thr Asp Asp Leu Val Arg Asn Ser Asn
 262 85 90 95
 266 Lys Thr Met Val Leu Thr Glu Ile Lys Thr Ile Thr Glu Phe Ala Thr
 268 100 105 110
 272 Thr Thr Val Ser Pro Thr Gln Glu Phe Gln Ala Leu Gln Ile Asn Leu
 274 115 120 125
 278 Asn Thr Leu Ser Ile Glu Thr Ser Thr Pro Thr Phe Gln Ser His Asp
 280 130 135 140
 284 Phe Pro Pro Ile Thr Ile Glu Asp Thr Pro Lys Thr Leu Glu Pro Glu
 286 145 150 155 160
 290 Glu Ser Ser Asp Ala Leu Gln Arg Asp Ala Phe Asp Gln Ile Lys Lys
 292 165 170 175
 296 Leu Glu Lys Leu Val Leu Asp Leu Arg Leu Glu Met Lys Glu Gln Gln
 298 180 185 190
 302 Lys Ser Phe Asn Asp Gln Leu Val Asp Ile Tyr Thr Ala Arg Ser Ile
 304 195 200 205
 308 Val Pro Ile Tyr Thr His Ile Val Thr Ser Ala Ile Pro Ser Tyr
 310 210 215 220
 314 Val Pro Lys Glu Glu Val Met Val Ser His Asp Thr Ala Pro Ile Val
 316 225 230 235 240
 320 Ser Arg Pro Arg Thr Asp Ile Pro Val Ser Gln Arg Ile Asp Thr Ile
 322 245 250 255
 326 Ser Lys His Lys Met Asn Gly Lys Asn Ile Leu Asn Asn Pro Pro
 328 260 265 270
 332 Pro Asn Ser Val Leu Ile Val Pro Gln Phe Gln Phe His Glu Arg Met
 334 275 280 285
 338 Ala Thr Lys Thr Glu Val Ala Tyr Met Lys Pro Lys Ile Val Trp Thr
 340 290 295 300
 344 Asn Phe Pro Thr Thr Ala Thr Ser Met Phe Asp Asn Phe Ile Leu
 346 305 310 315 320
 350 Lys Asn Leu Val Asp Glu Thr Asp Ser Glu Ile Asp Ser Gly Glu Thr
 352 325 330 335

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/763,011A

DATE: 11/14/2001
TIME: 13:52:05

Input Set : A:\JAB-1415.txt
Output Set: N:\CRF3\11142001\I763011A.raw

356 Glu Leu Ser Asp Asp Tyr Tyr Tyr Tyr Ser Tyr Glu Asp Asp Gly
358 340 345 350
362 Lys Glu Asp Asp Ser Asp Glu Ile Thr Ala Gln Ile Leu Leu Ser Asn
364 355 360 365
368 Ser Glu Leu Gly Thr Lys Thr Pro Asn Phe Glu Asp Pro Phe Glu Gln
370 370 375 380
374 Ile Asn Ile Glu Asp Asn Lys Val Ile Ser Val Asn Thr Pro Lys Thr
376 385 390 395 400
380 Lys Lys Pro Thr Thr Val Phe Gly Thr Ser Thr Ser Ala Leu Ser
382 405 410 415
386 Thr Phe Glu Ser Thr Ile Phe Glu Ile Pro Lys Phe Phe Tyr Gly Ser
388 420 425 430
392 Arg Arg Lys Gln Ser Ser Ser Phe Lys Asn Lys Asn Ser Thr Ile Lys
394 435 440 445
398 Phe Asp Val Phe Asp Trp Ile Phe Glu Ser Gly Thr Thr Asn Glu Lys
400 450 455 460
404 Val His Gly Leu Val Leu Val Ser Ser Gly Val Leu Leu Gly Thr Cys
406 465 470 475 480
410 Leu Leu Phe Ile Leu
412 485
418 <210> SEQ ID NO: 5
420 <211> LENGTH: 2193
422 <212> TYPE: DNA
424 <213> ORGANISM: Candida albicans
428 <400> SEQUENCE: 5

430 atgcaaccca cggtacaaca ctttaagatc cttagggatat ctccccacgtc aacatttagat 60
432 gaaatcaggga gggcataccg caaactatca ttgcgatacc accctgacaa aacaccacgt 120
434 cgagaagatc atgaaaaatt taaagagatc aatatacgat atgaaaacaat tagagattat 180
436 tatcaagaga atggggcaaaa gaacagtcaa ccgatcccta acacaaaacac agagcataat 240
438 tcccatcaaa aaccacatata taacactggc ccttatttca catatcgitt tacgacctca 300
440 tctaccacga ctgataatac caatcacact ggacattcaa gttctcggtt tacttattat 360
442 aattttcacc aaaaagcgcga agagaataac cgccaaacaag atgaagaaaag ggcagccaa 420
444 cgtgaacgtataaaaaagga gctttccag aggcaacaag cggagaagc acaacgaaaag 480
446 aaggaatttg aacaaaaggc cgaatttcataa aagcatcat tacttggaaat ggcggaaaga 540
448 gaaatagaga ggcggaaaca gcaaaaaggaa agggaaacaaa gacaaaagga gcacgaagca 600
450 aagagggata tcaggatatac acaacttca gagcaggatt cacggagtaa tcaaactaaa 660
452 gaagaagagg aagtgttcaa gaaggccccgg tctactaatt cgggagcaga cgagactgg 720
454 ttgatgtcag ataaagagtt tgatgattct gcatatttcac ccgatttattt gtttgaagag 780
456 aatttgtgga ataaacccaa tcatccagat acaaattcata aaacccaaaaa atataactgag 840
458 aatgtggttg aaaaatctaga ttctccacca aatgatacat ctgcgtacaa ttcaagttt 900
460 catgatgaaa ctaatattca aaatgagatc caaataccag aaaatgcga gtatgtacca 960
462 cagatgaaag ctacatccag tgtcaataat accaccatcc ctgcacaaag aagacatgag 1020
464 tcacttcca cttctgaaaa caaaaagaagg aaatttggaa cagccgacgt tggggttcat 1080
466 gggtagatt ccccagtgcg ggcacaacca gaaatatctg gaaaatccaa gtctccgata 1140
468 atccctgatg taataactttt actggacgaa gagactgaaa ctccctgaagc aaatgctgtg 1200
470 caggacaata gtacatataat tcctcagggg tcttttaggac acgaatttag aaatatttg 1260
472 gaagagcatac cacgtcaagt aaagaataaa caaaaattctg gtgttgctt tgcattccg 1320
474 aatgcttcca agaataccga aaacaaaactc cactctaatt tcaaagataa agatgaagga 1380
476 ataattgtat ttgaagctta cgtacctgat gtcaaagcag caacttcaaa caccacccca 1440

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/763,011A

DATE: 11/14/2001
TIME: 13:52:05

Input Set : A:\JAB-1415.txt
Output Set: N:\CRF3\11142001\I763011A.raw

478 gcaacaggac aaacatcagc aaggtcggaa aaactgccac ccttacctac tcatttcca 1500
 480 aatccatcga ccatgaatga agctcgacct catccaacaa ctccacataa aagatcaaaa 1560
 482 gtcattttcg attaaaaaga tttagaacaa aagtttaggtt atgatattga ggatttggat 1620
 484 tttaaggata tgtatgagag tttgcctgac cattcaagta aggcaacacc taaagacgat 1680
 486 attttaaccc gttctaaaag aagactttat acatataccg atggaacatc aaaggctgaa 1740
 488 acgttatcta caccaatgaa caaaaatctt gttcgtggac atagtaccaa gaaaaagctt 1800
 490 agtatgttgg acatgcattgc gtcttctaaa attcaaagtc ttttacctcc acaaccgcca 1860
 492 caaatgtcaa ttgatccttc tggttccaag caagtgtggg ctaaatacgt tgatgcaatc 1920
 494 ttgacttatac aaagagaatt ttcaattat aaaaaagtga ttgttcaata ccaaattggaa 1980
 496 cggataaaaca aagaccttga acatttgac gatataaatg atggttcaca cactgagaat 2040
 498 ttggatactt tcaagcattt tttagaacaa gattatttgg ttatgagtga gtttaatgaa 2100
 500 gcgttacgac aatttggta caccattgcc acgtatcagc aaaacctcca gtgggttaac 2160
 502 actttcatgg aaagggatcc taattggcta taa 2193
 506 <210> SEQ ID NO: 6
 508 <211> LENGTH: 730
 510 <212> TYPE: PRT
 512 <213> ORGANISM: Candida albicans
 516 <400> SEQUENCE: 6
 518 Met Gln Pro Thr Val Gln His Phe Lys Ile Leu Gly Ile Ser Pro Thr
 1 5 10 15
 520 Ser Thr Leu Asp Glu Ile Arg Arg Ala Tyr Arg Lys Leu Ser Leu Arg
 20 25 30
 524 Tyr His Pro Asp Lys Thr Pro Arg Arg Glu Asp His Glu Lys Phe Lys
 35 40 45
 526 Glu Ile Asn Ile Ala Tyr Glu Thr Ile Arg Asp Tyr Tyr Gln Glu Asn
 50 55 60
 530 Gly Gln Lys Asn Ser Gln Pro Ile Pro Asn Thr Asn Thr Glu His Asn
 65 70 75 80
 532 Ser His Gln Lys Pro His Tyr Asn Thr Gly Pro Tyr Ser Thr Tyr Arg
 85 90 95
 534 Phe Thr Thr Ser Ser Thr Thr Asp Asn Thr Asn His Thr Gly His
 100 105 110
 536 Ser Ser Ser Arg Phe Thr Tyr Tyr Asn Phe His Gln Lys Ala Gln Glu
 115 120 125
 540 Asn Asn Arg Lys Gln Asp Glu Glu Arg Ala Ala Gln Arg Glu Arg Leu
 130 135 140
 542 Lys Lys Glu Leu Phe Gln Arg Gln Gln Ala Glu Glu Ala Gln Arg Lys
 145 150 155 160
 544 Lys Glu Phe Glu Gln Lys Ala Glu Phe Ile Lys Ala Ser Leu Leu Glu
 165 170 175
 546 Met Arg Arg Arg Glu Ile Glu Arg Arg Lys Gln Gln Lys Glu Arg Glu
 180 185 190
 548 Gln Arg Gln Lys Glu His Glu Ala Lys Arg Asp Ile Arg Ile Gln Gln
 195 200 205
 550 Leu Ser Glu Gln Asp Ser Arg Ser Asn Gln Thr Lys Glu Glu Glu
 210 215 220
 552 Val Phe Lys Lys Ala Arg Ser Thr Asn Ser Gly Ala Asp Glu Thr Gly
 225 230 235 240
 554 Leu Met Ser Asp Lys Glu Phe Asp Asp Ser Ala Tyr Ser Pro Asp Tyr

09/76 3011A

Page 5 of 7B

?10> 13

?11> 302

?12> PRT

?13> Candida albicans

?20>

?21> Xaa = any amino acid at positions 58 and 185

**Does Not Comply
Corrected Diskette Needed**

1. Unknowns must be enumerated on fields 221 222 and 223.
2. Field 221 as "variant"
3. Field 222 as location "58 and 185"
4. Field 223 as particular amino acids

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/763,011A

DATE: 11/14/2001
TIME: 13:52:06

Input Set : A:\JAB-1415.txt
Output Set: N:\CRF3\11142001\I763011A.raw

19 M:270 C: Current Application Number differs, Replaced Application Number
21 M:271 C: Current Filing Date differs, Replaced Current Filing Date
1041 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
1067 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
1067 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
1067 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
1115 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
1115 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
1115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
5512 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:57
5742 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:57
5742 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:57
5742 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57
5789 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:58
6635 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:58
6635 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:58
6635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58
13167 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:114
13330 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:114
13330 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:114
13330 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:114
13348 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:114
13348 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:114
13348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:114